SEQUENCE LISTING

<110> Osaka Industrial Promotion Organization
National Institure of Radiological Sciences
TAKEDA, Junji
HORIE, Kyoji
YUSA, Kosuke
ISHIHARA, Hiroshi

<120> Development of Mammalian Genome Modification Technique using Retrotransposon

<130> OT004US

<140> PCT/JP2004/017307
<141> 2004-11-19

<150> JP 2003-393175
<151> 2003-11-21

<160> 40

<170> PatentIn version 3.2

<210> 1
<211> 7318
<212> DNA
<213> Mus musculus

<220>
<223> IAP sequence actually used in the Examples for exemplification

<220>
<221> CDS
<222> (670)..(2427)

<220>
<221> CDS
<222> (2430)..(3203)

<220>
<221> CDS
<222> (3440)..(5854)

<400> 1
tgtgggaagc cgcccccaca ttcgccgtca caagatggtg ctgacatcct gtgttctaag 60

ttggtaaaca aataatctgc gcatgagcca agggtattta cgactacttg tactctgttt 120

ttcccgtgaa cgtcagctcg gccatgggct gcagccaatc agggagtgat gcgccctagg 180

caatggttgt tctctttaaa atagaagggg tttcgttttt ctcgctctct tgcttcttgc 240

tctctcttgc ttccctctct tgcttcttgc tctctcttgc ttccctctct tgcttcttgc 300

tctctcttgc ttccctctct tgcttcttgc tctctcttgc ttcttgctct cttttcctga 360

agatgtaaga ataaagcttt gtcgcagaag attctggtct gtggtgttct tcctggccgg 420

tcgtgagaac gcgtcgaata acaattggtg ccgaattccg ggacgagaaa atccgggacg 480

```
agaaaaaact ccggactggc gcaggaggga tacttcattt cagaaccaga actacggatc    540

acgtttataa aggttcccgt aacacagact gttgagaagg attcaactgc cgaattcaga    600

actcatcagc tggggaacga cggtgataaa ggttcccgta aagcagactg ttaaaaagga    660

ttcaactgt atg aat tca gaa ctt ttc agc tgg gga acg aga gta cca gtg     711
          Met Asn Ser Glu Leu Phe Ser Trp Gly Thr Arg Val Pro Val
          1               5                   10

agt atg ttt ggc ctt gaa ttt ttt ctg gtg tta gga gcc ctt ttg ttc      759
Ser Met Phe Gly Leu Glu Phe Phe Leu Val Leu Gly Ala Leu Leu Phe
15                  20                  25                  30

ctt ttc aca tgt tat ata gtg gtt aag gca ggg ctg aaa att ctg gat      807
Leu Phe Thr Cys Tyr Ile Val Val Lys Ala Gly Leu Lys Ile Leu Asp
                35                  40                  45

gaa att cag ggc agt cta tca gaa gta aag cgg gga gag aga gta gga      855
Glu Ile Gln Gly Ser Leu Ser Glu Val Lys Arg Gly Glu Arg Val Gly
            50                  55                  60

gca agg aga aac ggt aag tat aca ggc ctt tcc aag ggt ctt gaa ccc      903
Ala Arg Arg Asn Gly Lys Tyr Thr Gly Leu Ser Lys Gly Leu Glu Pro
        65                  70                  75

gag gaa aag tta agg tta ggt agg aat acc tgg aga gag att aga aga      951
Glu Glu Lys Leu Arg Leu Gly Arg Asn Thr Trp Arg Glu Ile Arg Arg
    80                  85                  90

aaa aga gga aaa agg gaa aag aaa aaa gat cga tta gcg gag gtc tct      999
Lys Arg Gly Lys Arg Glu Lys Lys Lys Asp Arg Leu Ala Glu Val Ser
95                  100                 105                 110

agg aga tac tcg tca cta gat gag ctc agg aag cca gct ctt agt agc     1047
Arg Arg Tyr Ser Ser Leu Asp Glu Leu Arg Lys Pro Ala Leu Ser Ser
                115                 120                 125

tct gaa gca agt gaa gaa tcc tcc tct gag gaa aca gac tgg gag gaa     1095
Ser Glu Ala Ser Glu Glu Ser Ser Ser Glu Glu Thr Asp Trp Glu Glu
            130                 135                 140

gaa gca gcc cat tac cag cca gct aat tgg tca aga aaa aag cca aaa     1143
Glu Ala Ala His Tyr Gln Pro Ala Asn Trp Ser Arg Lys Lys Pro Lys
        145                 150                 155

gcg gct ggc gaa agt cag cgt act gtt caa cct ccc ggc agt cgg ttt     1191
Ala Ala Gly Glu Ser Gln Arg Thr Val Gln Pro Pro Gly Ser Arg Phe
    160                 165                 170

caa ggt ccg ccc tat gcg gag ccc ccg ccc tgc gta gtg cgt cag caa     1239
Gln Gly Pro Pro Tyr Ala Glu Pro Pro Pro Cys Val Val Arg Gln Gln
175                 180                 185                 190

tgc gca gag agg caa tgc gca gag agg tgc gca gag agg cag tgc gca     1287
Cys Ala Glu Arg Gln Cys Ala Glu Arg Cys Ala Glu Arg Gln Cys Ala
                195                 200                 205

gac agg tgc gca gag agg cag tgc gca gag agg cag tgc gca gac tca     1335
Asp Arg Cys Ala Glu Arg Gln Cys Ala Glu Arg Gln Cys Ala Asp Ser
```

```
            210                 215                 220

ttc att ccc cga gag gaa caa aag aaa ata gaa cag gca ttt cca gtc     1383
Phe Ile Pro Arg Glu Glu Gln Lys Lys Ile Glu Gln Ala Phe Pro Val
        225                 230                 235

ttt gaa gga gcc gag ggt ggg cgt gtc cac gct ccg gta gaa tac gta     1431
Phe Glu Gly Ala Glu Gly Gly Arg Val His Ala Pro Val Glu Tyr Val
    240                 245                 250

cag att aag gaa att gcc gag tcg gtt cgt aaa tac gga acc aat gct     1479
Gln Ile Lys Glu Ile Ala Glu Ser Val Arg Lys Tyr Gly Thr Asn Ala
255                 260                 265                 270

aat ttc acc ttg gtg cag tta gac agg ctc gct ggt atg gca cta acg     1527
Asn Phe Thr Leu Val Gln Leu Asp Arg Leu Ala Gly Met Ala Leu Thr
                275                 280                 285

cct gct gat tgg cag acg gtt gta aaa gcc gct ctt cct agt atg ggc     1575
Pro Ala Asp Trp Gln Thr Val Val Lys Ala Ala Leu Pro Ser Met Gly
            290                 295                 300

aaa tat atg gaa tgg aaa gcg ctt tgg cac gaa gct gca cag gcg cag     1623
Lys Tyr Met Glu Trp Lys Ala Leu Trp His Glu Ala Ala Gln Ala Gln
        305                 310                 315

gcc cga gca aac gca gct gct ttg act cca gag cag aga gat tgg act     1671
Ala Arg Ala Asn Ala Ala Ala Leu Thr Pro Glu Gln Arg Asp Trp Thr
    320                 325                 330

ttt gac ttg tta acg ggt cag gga gct tat tct gct gat cag aca aac     1719
Phe Asp Leu Leu Thr Gly Gln Gly Ala Tyr Ser Ala Asp Gln Thr Asn
335                 340                 345                 350

tac cat tgg gga gct tat gcc cag att tct tcc acg gct att agg gcc     1767
Tyr His Trp Gly Ala Tyr Ala Gln Ile Ser Ser Thr Ala Ile Arg Ala
                355                 360                 365

tgg aag gcg ctc tct cga gca ggt gaa acc act ggt cag tta aca aaa     1815
Trp Lys Ala Leu Ser Arg Ala Gly Glu Thr Thr Gly Gln Leu Thr Lys
            370                 375                 380

ata atc cag gga cct cag gaa tct ttc tca gat ttt gtg gcc aga atg     1863
Ile Ile Gln Gly Pro Gln Glu Ser Phe Ser Asp Phe Val Ala Arg Met
        385                 390                 395

aca gag gca gca gag cgt att ttt gga gag tca gag caa gct gcg cct     1911
Thr Glu Ala Ala Glu Arg Ile Phe Gly Glu Ser Glu Gln Ala Ala Pro
    400                 405                 410

ctc ata gaa cag cta atc tac gag caa gcc aca aag gag tgc cga gcg     1959
Leu Ile Glu Gln Leu Ile Tyr Glu Gln Ala Thr Lys Glu Cys Arg Ala
415                 420                 425                 430

gcc ata gcc cca aga aag aac aaa ggc tta caa gac tgg ctc agg gtc     2007
Ala Ile Ala Pro Arg Lys Asn Lys Gly Leu Gln Asp Trp Leu Arg Val
                435                 440                 445

tgt cga gag ctt ggg gga ccc ctt agc aat gca ggt tta gcg gct gcc     2055
Cys Arg Glu Leu Gly Gly Pro Leu Ser Asn Ala Gly Leu Ala Ala Ala
            450                 455                 460
```

```
atc ctt caa tcc caa aac cgc tcc atg ggc aga aat gat cag agg aca     2103
Ile Leu Gln Ser Gln Asn Arg Ser Met Gly Arg Asn Asp Gln Arg Thr
        465                 470                 475

tgt ttt aac tgc gga aag cct ggg cat ttt aag aaa gat tgc aga gct     2151
Cys Phe Asn Cys Gly Lys Pro Gly His Phe Lys Lys Asp Cys Arg Ala
    480                 485                 490

cca gat aaa cag gga ggg act ctc act ctt tgc tct aag tgt ggc aag     2199
Pro Asp Lys Gln Gly Gly Thr Leu Thr Leu Cys Ser Lys Cys Gly Lys
495                 500                 505                 510

ggt tat cat aga gct gac cag tgt cgc tct gtg agg gat ata aag ggc     2247
Gly Tyr His Arg Ala Asp Gln Cys Arg Ser Val Arg Asp Ile Lys Gly
                515                 520                 525

aga att ctt ccc cca cct gat agt caa tca gct gat gtg cca aaa aac     2295
Arg Ile Leu Pro Pro Pro Asp Ser Gln Ser Ala Asp Val Pro Lys Asn
            530                 535                 540

ggg tca ccg ggc cct cgg tcc cag ggc cct caa aga tat ggg aac cgg     2343
Gly Ser Pro Gly Pro Arg Ser Gln Gly Pro Gln Arg Tyr Gly Asn Arg
        545                 550                 555

ttt gtc agg acc cag gaa gca gtc aga gag acg acc cag gaa gac cca     2391
Phe Val Arg Thr Gln Glu Ala Val Arg Glu Thr Thr Gln Glu Asp Pro
    560                 565                 570

caa ggg tgg acc tgc gtg ccg cct ccg act tcc tat ta atg cct caa      2438
Gln Gly Trp Thr Cys Val Pro Pro Pro Thr Ser Tyr    Met Pro Gln
575                 580                 585

atg agt att cag ccg gtg ccg gtg gag cct ata cca tcc ttg ccc ccg     2486
Met Ser Ile Gln Pro Val Pro Val Glu Pro Ile Pro Ser Leu Pro Pro
590                 595                 600                 605

gga acc atg ggc ctt att ctc ggc cga ggt tca ctc acc ttg cag ggc     2534
Gly Thr Met Gly Leu Ile Leu Gly Arg Gly Ser Leu Thr Leu Gln Gly
                610                 615                 620

tta gta gtc cac cct gga att atg gat tgt caa cat tcc cct gaa ata     2582
Leu Val Val His Pro Gly Ile Met Asp Cys Gln His Ser Pro Glu Ile
            625                 630                 635

cag gtc ctg tgc tca agc cct aaa ggc gtt ttt tct att agt aaa gga     2630
Gln Val Leu Cys Ser Ser Pro Lys Gly Val Phe Ser Ile Ser Lys Gly
        640                 645                 650

gat agg ata gct cag ctg ctg ctc ctc cct gat aat acc agg gag aaa     2678
Asp Arg Ile Ala Gln Leu Leu Leu Leu Pro Asp Asn Thr Arg Glu Lys
    655                 660                 665

tct gca gga cct gag ata aag aaa atg ggc tcc tca gga aat gat tct     2726
Ser Ala Gly Pro Glu Ile Lys Lys Met Gly Ser Ser Gly Asn Asp Ser
670                 675                 680                 685

gcc tat ttg gtt gta tct tta aat gat aga cct aag ctc cgc ctt aag     2774
Ala Tyr Leu Val Val Ser Leu Asn Asp Arg Pro Lys Leu Arg Leu Lys
                690                 695                 700
```

```
att aat gga aaa gag ttt gaa ggc atc ctt gat acc gga gca gat aaa     2822
Ile Asn Gly Lys Glu Phe Glu Gly Ile Leu Asp Thr Gly Ala Asp Lys
            705                 710                 715

agt ata att tct aca cat tgg tgg ccc aaa gca tgg ccc acc aca gag     2870
Ser Ile Ile Ser Thr His Trp Trp Pro Lys Ala Trp Pro Thr Thr Glu
        720                 725                 730

tca tct cat tca tta cag ggc cta gga tat caa tca tgt ccc act ata     2918
Ser Ser His Ser Leu Gln Gly Leu Gly Tyr Gln Ser Cys Pro Thr Ile
    735                 740                 745

agc tcc gtt gcc ttg acg tgg gaa tcc tct gaa ggg cag caa ggg aaa     2966
Ser Ser Val Ala Leu Thr Trp Glu Ser Ser Glu Gly Gln Gln Gly Lys
750                 755                 760                 765

ttc ata cct tat gtg ctc cca ctc ccg gtt aac ctc tgg gga agg gat     3014
Phe Ile Pro Tyr Val Leu Pro Leu Pro Val Asn Leu Trp Gly Arg Asp
                770                 775                 780

att atg cag cat ttg ggc ctt att ttg tcc aat gaa aac gcc cca tca     3062
Ile Met Gln His Leu Gly Leu Ile Leu Ser Asn Glu Asn Ala Pro Ser
            785                 790                 795

gga ggg tat tca gct aaa gca aaa aat atc atg gca aag atg ggt tat     3110
Gly Gly Tyr Ser Ala Lys Ala Lys Asn Ile Met Ala Lys Met Gly Tyr
        800                 805                 810

aaa gaa gga aaa ggg tta gga cat caa gaa cag gga agg ata gag ccc     3158
Lys Glu Gly Lys Gly Leu Gly His Gln Glu Gln Gly Arg Ile Glu Pro
    815                 820                 825

atc tca cct aat gga aac caa gac aga cag ggt ctg ggt ttt cca         3203
Ile Ser Pro Asn Gly Asn Gln Asp Arg Gln Gly Leu Gly Phe Pro
830                 835                 840

tagcggccat tggggcagca cgacccatac catggaaaac aggggaccca gtgtgggttc   3263

ctcaatggca cctatcctct gaaaaactag aagctgtgat tcaactggta gaggaacaat   3323

taaaattagg ccatattgaa ccctctacct caccttggaa tactccaatt tttgtaatta   3383

agaaaaagtc aggaaagtgg agactgctcc atgacctcag agccattaat gagcaa atg   3442
                                                              Met
                                                              845

aac tta ttt ggc cca gta cag agg ggt ctc cct gta ctt tcc gcc tta     3490
Asn Leu Phe Gly Pro Val Gln Arg Gly Leu Pro Val Leu Ser Ala Leu
                850                 855                 860

cca cgt ggc tgg aat tta atc att ata gat att aaa gat tgt ttc ttt     3538
Pro Arg Gly Trp Asn Leu Ile Ile Ile Asp Ile Lys Asp Cys Phe Phe
            865                 870                 875

tct ata cct ttg tgt cca agg gat agg ccc aga ttt gcc ttt acc atc     3586
Ser Ile Pro Leu Cys Pro Arg Asp Arg Pro Arg Phe Ala Phe Thr Ile
        880                 885                 890

ccc tct att aat cac atg gaa cct gat aag agg tat caa tgg aag gtc     3634
Pro Ser Ile Asn His Met Glu Pro Asp Lys Arg Tyr Gln Trp Lys Val
    895                 900                 905
```

```
tta cca cag gga atg tcc aat agt cct act atg tgt caa ctt tat gta     3682
Leu Pro Gln Gly Met Ser Asn Ser Pro Thr Met Cys Gln Leu Tyr Val
910                 915                 920                 925

caa gaa gct ctt ttg cca gtg agg gaa caa ttc ccc tct tta att ttg     3730
Gln Glu Ala Leu Leu Pro Val Arg Glu Gln Phe Pro Ser Leu Ile Leu
                930                 935                 940

ctc ctt tac atg gat gac atc ctc ctg tgc cat aaa gac ctt acc atg     3778
Leu Leu Tyr Met Asp Asp Ile Leu Leu Cys His Lys Asp Leu Thr Met
            945                 950                 955

cta caa aag gca tat cct ttt cta ctt aaa act tta agt cag tgg ggt     3826
Leu Gln Lys Ala Tyr Pro Phe Leu Leu Lys Thr Leu Ser Gln Trp Gly
        960                 965                 970

cta cag ata gcc aca gaa aag gtc caa att tct gat aca gga caa ttc     3874
Leu Gln Ile Ala Thr Glu Lys Val Gln Ile Ser Asp Thr Gly Gln Phe
    975                 980                 985

ttg ggc tct gtg gtg tcc cca gat aag att gtg  ccc caa aag gta gag    3922
Leu Gly Ser Val Val Ser Pro Asp Lys Ile Val  Pro Gln Lys Val Glu
990                 995                 1000                1005

ata aga aga gat cac  ctc cat acc tta aat  gat ttt caa aag ctg       3967
Ile Arg Arg Asp His  Leu His Thr Leu Asn  Asp Phe Gln Lys Leu
                1010                1015                1020

ttg gga gat att aat  tgg ctc aga ccc ttt  tta aag att cct tct       4012
Leu Gly Asp Ile Asn  Trp Leu Arg Pro Phe  Leu Lys Ile Pro Ser
                1025                1030                1035

gct gaa tta agg cct  ttg ttt agt att tta  gaa gga gat cct cat       4057
Ala Glu Leu Arg Pro  Leu Phe Ser Ile Leu  Glu Gly Asp Pro His
                1040                1045                1050

atc tcc tcc cct agg  act ctt act cta gct  gct aac cag gcc tta       4102
Ile Ser Ser Pro Arg  Thr Leu Thr Leu Ala  Ala Asn Gln Ala Leu
                1055                1060                1065

caa aaa gtg gaa aaa  gcc tta cag aat gca  caa tta caa cgt att       4147
Gln Lys Val Glu Lys  Ala Leu Gln Asn Ala  Gln Leu Gln Arg Ile
                1070                1075                1080

gag gat tcg cag cct  ttc agt ttg tgt gtc  ttt aag aca gca caa       4192
Glu Asp Ser Gln Pro  Phe Ser Leu Cys Val  Phe Lys Thr Ala Gln
                1085                1090                1095

ttg cca act gca gtt  ttg tgg cag aat ggg  cca ttg ttg tgg atc       4237
Leu Pro Thr Ala Val  Leu Trp Gln Asn Gly  Pro Leu Leu Trp Ile
                1100                1105                1110

cat cca aac gta tcc  cca gct aaa ata ata  gat tgg tat cct gat       4282
His Pro Asn Val Ser  Pro Ala Lys Ile Ile  Asp Trp Tyr Pro Asp
                1115                1120                1125

gca att gca cag ctt  gcc ctt aaa ggc cta  aaa gca gca atc acc       4327
Ala Ile Ala Gln Leu  Ala Leu Lys Gly Leu  Lys Ala Ala Ile Thr
                1130                1135                1140
```

```
cac ttt ggg caa agt  cca tat ctt tta att  gta cct tat acc gct       4372
His Phe Gly Gln Ser  Pro Tyr Leu Leu Ile  Val Pro Tyr Thr Ala
                1145                1150                1155

gca cag gtt caa acc  ttg gca gcc gca tct  aat gat tgg gca gtt       4417
Ala Gln Val Gln Thr  Leu Ala Ala Ala Ser  Asn Asp Trp Ala Val
                1160                1165                1170

tta gtt acc tcc ttt  tca gga aaa ata gat  aac cat tat cca aag       4462
Leu Val Thr Ser Phe  Ser Gly Lys Ile Asp  Asn His Tyr Pro Lys
                1175                1180                1185

cat cca atc tta cag  ttt gcc caa aat caa  tct gtt gtg ttt cca       4507
His Pro Ile Leu Gln  Phe Ala Gln Asn Gln  Ser Val Val Phe Pro
                1190                1195                1200

caa ata aca gta aga  aac cca ctt aaa aat  ggg att gtg gta tat       4552
Gln Ile Thr Val Arg  Asn Pro Leu Lys Asn  Gly Ile Val Val Tyr
                1205                1210                1215

act gat gga tca aaa  act ggc ata ggt gcc  tat gtg gct aat ggt       4597
Thr Asp Gly Ser Lys  Thr Gly Ile Gly Ala  Tyr Val Ala Asn Gly
                1220                1225                1230

aaa gtg gta tcc aaa  cag tat aat gaa aat  tca cct caa gtg gta       4642
Lys Val Val Ser Lys  Gln Tyr Asn Glu Asn  Ser Pro Gln Val Val
                1235                1240                1245

gaa tgt tta gtg gtc  tta gaa gtt tta aaa  acc ttt tta aaa ccc       4687
Glu Cys Leu Val Val  Leu Glu Val Leu Lys  Thr Phe Leu Lys Pro
                1250                1255                1260

ctt aat att gtg tca  gat tcc tgt tat gtg  gta aat gca gta aat       4732
Leu Asn Ile Val Ser  Asp Ser Cys Tyr Val  Val Asn Ala Val Asn
                1265                1270                1275

ctt tta gaa gtg gct  gga gtg att aag cct  tcc agt aga gtt gcc       4777
Leu Leu Glu Val Ala  Gly Val Ile Lys Pro  Ser Ser Arg Val Ala
                1280                1285                1290

aat att ttt cag cag  ata caa tta gtt ttg  tta tct aga aga tct       4822
Asn Ile Phe Gln Gln  Ile Gln Leu Val Leu  Leu Ser Arg Arg Ser
                1295                1300                1305

cct gtt tat att act  cat gtt aga gcc cat  tca ggc cta cct ggc       4867
Pro Val Tyr Ile Thr  His Val Arg Ala His  Ser Gly Leu Pro Gly
                1310                1315                1320

ccc atg gct ctg gga  aat gat ttg gca gat  aag gcc act aaa gtg       4912
Pro Met Ala Leu Gly  Asn Asp Leu Ala Asp  Lys Ala Thr Lys Val
                1325                1330                1335

gtg gct gct gcc cta  tca tcc ccg gta gag  gct gca aga aat ttt       4957
Val Ala Ala Ala Leu  Ser Ser Pro Val Glu  Ala Ala Arg Asn Phe
                1340                1345                1350

cat aat aat ttt cat  gtg acg gct gaa aca  tta cgc agt cgt ttc       5002
His Asn Asn Phe His  Val Thr Ala Glu Thr  Leu Arg Ser Arg Phe
                1355                1360                1365

tcc ttg aca aga aaa  gaa gcc cgt gac att  gtt act caa tgt caa       5047
```

```
Ser Leu Thr Arg Lys  Glu Ala Arg Asp Ile  Val Thr Gln Cys Gln
                1370                1375                1380

agc tgc tgt gag ttc  ttg cca gtt cct cat  gtg gga att aac cca       5092
Ser Cys Cys Glu Phe  Leu Pro Val Pro His  Val Gly Ile Asn Pro
                1385                1390                1395

cgc ggt att cga cct  cta cag gtc tgg caa  atg gat gtt aca cat       5137
Arg Gly Ile Arg Pro  Leu Gln Val Trp Gln  Met Asp Val Thr His
                1400                1405                1410

gtt tct tcc ttt gga  aaa ctt caa tat ctc  cat gtg tcc att gac       5182
Val Ser Ser Phe Gly  Lys Leu Gln Tyr Leu  His Val Ser Ile Asp
                1415                1420                1425

aca tgt tct ggc atc  atg ttt gct tct ccg  tta act gga gaa aaa       5227
Thr Cys Ser Gly Ile  Met Phe Ala Ser Pro  Leu Thr Gly Glu Lys
                1430                1435                1440

gcc tca cat gtg att  caa cat tgt ctt gag  gca tgg agt gct tgg       5272
Ala Ser His Val Ile  Gln His Cys Leu Glu  Ala Trp Ser Ala Trp
                1445                1450                1455

ggg aaa ccc aga ctc  ctt aag act gat aat  gga cca gct tat acg       5317
Gly Lys Pro Arg Leu  Leu Lys Thr Asp Asn  Gly Pro Ala Tyr Thr
                1460                1465                1470

tcc caa aaa ttt cag  cag ttc tgc cgt cag  atg gac gta acc cac       5362
Ser Gln Lys Phe Gln  Gln Phe Cys Arg Gln  Met Asp Val Thr His
                1475                1480                1485

ctg act gga ctt cca  tac aac cct caa gga  cag ggt att gtt gag       5407
Leu Thr Gly Leu Pro  Tyr Asn Pro Gln Gly  Gln Gly Ile Val Glu
                1490                1495                1500

cgt gcg cat cgc acc  ctc aaa gcc tat ctt  ata aaa cag aag agg       5452
Arg Ala His Arg Thr  Leu Lys Ala Tyr Leu  Ile Lys Gln Lys Arg
                1505                1510                1515

gga act ttt gag gag  act gta ccc cga gca  cca aga gtg tcg gtg       5497
Gly Thr Phe Glu Glu  Thr Val Pro Arg Ala  Pro Arg Val Ser Val
                1520                1525                1530

tct ttg gca ctc ttt  aca ctc aat ttt tta  aat att gat gct cat       5542
Ser Leu Ala Leu Phe  Thr Leu Asn Phe Leu  Asn Ile Asp Ala His
                1535                1540                1545

ggc cat act gcg gct  gaa cgt cat tgt tca  gag cca gat agg ccc       5587
Gly His Thr Ala Ala  Glu Arg His Cys Ser  Glu Pro Asp Arg Pro
                1550                1555                1560

aat gag atg gtt aaa  tgg aaa aat gtc ctt  gat aat aaa tgg tat       5632
Asn Glu Met Val Lys  Trp Lys Asn Val Leu  Asp Asn Lys Trp Tyr
                1565                1570                1575

ggc ccg gat cct atc  ttg ata aga tcc agg  gga gct atc tgt gtt       5677
Gly Pro Asp Pro Ile  Leu Ile Arg Ser Arg  Gly Ala Ile Cys Val
                1580                1585                1590

ttc cca cag aat gaa  gac aac cca ttt tgg  gta cca gaa aga ctc       5722
Phe Pro Gln Asn Glu  Asp Asn Pro Phe Trp  Val Pro Glu Arg Leu
```

```
                1595                1600                1605

acc cga aaa atc cag  act gac caa ggg aat  act aat gtc cct cgt       5767
Thr Arg Lys Ile Gln  Thr Asp Gln Gly Asn  Thr Asn Val Pro Arg
                1610                1615                1620

ctt ggt gat gtc cag  ggc gtc aat aat aaa  gag aga gca gcg ttg       5812
Leu Gly Asp Val Gln  Gly Val Asn Asn Lys  Glu Arg Ala Ala Leu
                1625                1630                1635

ggg gat aat gtc gac  att tcc act ccc aat  gac ggt gat gta           5854
Gly Asp Asn Val Asp  Ile Ser Thr Pro Asn  Asp Gly Asp Val
                1640                1645

taatgctcaa gtattctcct gctttttac cactaactag gaactgggtt tggccttaat   5914

tcagacagcc ttggctctgt ctggacaggt ccagatgact gacaccatta acactttgtc   5974

agcctcagtg actacagtca tagatgaaca ggcctcagct aatgtcaaga tacagagagg   6034

tctcatgctg gttaatcaac tcatagatct tgtccagaaa caactggatg tattatgaca   6094

aataactcag cagggatgtg aacaaaagtt tccgggattg tgtgttattt ccattcagta   6154

tgttaaattt actaggacag ctaatttgtc aaaaagtctt tttcagtata tgttacagaa   6214

ttggatggct gaatttgaat agatccttcg agaattgaga cttcaggtca actccacgcg   6274

cttggacctg tcgctgacca aaagattacc caattggatc tcctcagcat tttctttctt   6334

taaaaaattg ggtgggatta atattatttg gagatacact ttgctgtgga ttagtgttgc   6394

ttctttgatt ggtctgtaag cttaaggccc aaactaagag agacaaggtg gttattgccc   6454

aggcgcttgc aggactagaa catggagctt cccctgatat atctatgctt aagcaatagg   6514

tcgctggcca ctcagctctt atatctcacg aggctagtct cattgcacga gatagagtga   6574

gtgtgcttca gcagcccgag agagttgcaa ggctaagcac tgcagtagaa gggctctgcg   6634

gcacatatga gcctattcta gggagacatg tcatctttca tgaaggttca gtgtcctagt   6694

tcccttcccc caggcaaaac gacacgggag caggtcaggg ttgctctggg taaaagcctg   6754

taagcctaag agctaatcct gtacatggct cctttaccta cacactgggg atttgacctc   6814

tatctccact ctcattaata tgggtggcct atttgctctt attaaaagaa aaaggggaa    6874

ctgtgggaag ccgcccccac attcgccgtc acaagatggc gctgacatcc tgtgttctaa   6934

gttggtaaac aaataatctg cgcatgagcc aagggtattt acgactactt gtactctgtt   6994

tttcccgtga acgtcagctc ggccatgggc tgcagccaat cagggagtga tgcgccctag   7054

gcaatggttg ttctctttaa aatagaaggg gtttcgtttt tctcgctctc ttgcttcttg   7114

ctctctcttg cttccctctc ttgcttcttg ctctctcttg cttccctctc ttgcttcttg   7174

ctctctcttg cttccctctc ttgcttcttg ctctctcttg cttcttgctc tcttttcctg   7234

aagatgtaag aataaagctt tgtcgcagaa gattctggtc tgtggtgttc ttcctggccg   7294
```

gtcgtgagaa cgcgtcgaat aaca 7318

<210> 2
<211> 586
<212> PRT
<213> Mus musculus

<220>
<223> IAP sequence amino acid sequence (gag #1)

<400> 2

Met Asn Ser Glu Leu Phe Ser Trp Gly Thr Arg Val Pro Val Ser Met
1 5 10 15

Phe Gly Leu Glu Phe Phe Leu Val Leu Gly Ala Leu Leu Phe Leu Phe
20 25 30

Thr Cys Tyr Ile Val Val Lys Ala Gly Leu Lys Ile Leu Asp Glu Ile
35 40 45

Gln Gly Ser Leu Ser Glu Val Lys Arg Gly Glu Arg Val Gly Ala Arg
50 55 60

Arg Asn Gly Lys Tyr Thr Gly Leu Ser Lys Gly Leu Glu Pro Glu Glu
65 70 75 80

Lys Leu Arg Leu Gly Arg Asn Thr Trp Arg Glu Ile Arg Arg Lys Arg
85 90 95

Gly Lys Arg Glu Lys Lys Lys Asp Arg Leu Ala Glu Val Ser Arg Arg
100 105 110

Tyr Ser Ser Leu Asp Glu Leu Arg Lys Pro Ala Leu Ser Ser Ser Glu
115 120 125

Ala Ser Glu Glu Ser Ser Ser Glu Glu Thr Asp Trp Glu Glu Glu Ala
130 135 140

Ala His Tyr Gln Pro Ala Asn Trp Ser Arg Lys Lys Pro Lys Ala Ala
145 150 155 160

Gly Glu Ser Gln Arg Thr Val Gln Pro Pro Gly Ser Arg Phe Gln Gly
165 170 175

Pro Pro Tyr Ala Glu Pro Pro Pro Cys Val Val Arg Gln Gln Cys Ala
180 185 190

```
Glu Arg Gln Cys Ala Glu Arg Cys Ala Glu Arg Gln Cys Ala Asp Arg
        195                 200                 205

Cys Ala Glu Arg Gln Cys Ala Glu Arg Gln Cys Ala Asp Ser Phe Ile
    210                 215                 220

Pro Arg Glu Glu Gln Lys Lys Ile Glu Gln Ala Phe Pro Val Phe Glu
225                 230                 235                 240

Gly Ala Glu Gly Gly Arg Val His Ala Pro Val Glu Tyr Val Gln Ile
                245                 250                 255

Lys Glu Ile Ala Glu Ser Val Arg Lys Tyr Gly Thr Asn Ala Asn Phe
            260                 265                 270

Thr Leu Val Gln Leu Asp Arg Leu Ala Gly Met Ala Leu Thr Pro Ala
        275                 280                 285

Asp Trp Gln Thr Val Val Lys Ala Ala Leu Pro Ser Met Gly Lys Tyr
    290                 295                 300

Met Glu Trp Lys Ala Leu Trp His Glu Ala Ala Gln Ala Gln Ala Arg
305                 310                 315                 320

Ala Asn Ala Ala Ala Leu Thr Pro Glu Gln Arg Asp Trp Thr Phe Asp
                325                 330                 335

Leu Leu Thr Gly Gln Gly Ala Tyr Ser Ala Asp Gln Thr Asn Tyr His
            340                 345                 350

Trp Gly Ala Tyr Ala Gln Ile Ser Ser Thr Ala Ile Arg Ala Trp Lys
        355                 360                 365

Ala Leu Ser Arg Ala Gly Glu Thr Thr Gly Gln Leu Thr Lys Ile Ile
    370                 375                 380

Gln Gly Pro Gln Glu Ser Phe Ser Asp Phe Val Ala Arg Met Thr Glu
385                 390                 395                 400

Ala Ala Glu Arg Ile Phe Gly Glu Ser Glu Gln Ala Ala Pro Leu Ile
                405                 410                 415

Glu Gln Leu Ile Tyr Glu Gln Ala Thr Lys Glu Cys Arg Ala Ala Ile
            420                 425                 430
```

```
Ala Pro Arg Lys Asn Lys Gly Leu Gln Asp Trp Leu Arg Val Cys Arg
        435                 440                 445

Glu Leu Gly Gly Pro Leu Ser Asn Ala Gly Leu Ala Ala Ala Ile Leu
    450                 455                 460

Gln Ser Gln Asn Arg Ser Met Gly Arg Asn Asp Gln Arg Thr Cys Phe
465                 470                 475                 480

Asn Cys Gly Lys Pro Gly His Phe Lys Lys Asp Cys Arg Ala Pro Asp
                485                 490                 495

Lys Gln Gly Gly Thr Leu Thr Leu Cys Ser Lys Cys Gly Lys Gly Tyr
            500                 505                 510

His Arg Ala Asp Gln Cys Arg Ser Val Arg Asp Ile Lys Gly Arg Ile
        515                 520                 525

Leu Pro Pro Pro Asp Ser Gln Ser Ala Asp Val Pro Lys Asn Gly Ser
    530                 535                 540

Pro Gly Pro Arg Ser Gln Gly Pro Gln Arg Tyr Gly Asn Arg Phe Val
545                 550                 555                 560

Arg Thr Gln Glu Ala Val Arg Glu Thr Thr Gln Glu Asp Pro Gln Gly
                565                 570                 575

Trp Thr Cys Val Pro Pro Pro Thr Ser Tyr
            580                 585
```

<210> 3
<211> 258
<212> PRT
<213> Mus musculus

<220>
<223> IAP sequence amino acid sequence (gag #2)

<400> 3

```
Met Pro Gln Met Ser Ile Gln Pro Val Pro Val Glu Pro Ile Pro Ser
1               5                   10                  15

Leu Pro Pro Gly Thr Met Gly Leu Ile Leu Gly Arg Gly Ser Leu Thr
            20                  25                  30

Leu Gln Gly Leu Val Val His Pro Gly Ile Met Asp Cys Gln His Ser
        35                  40                  45
```

```
Pro Glu Ile Gln Val Leu Cys Ser Ser Pro Lys Gly Val Phe Ser Ile
    50                  55                  60

Ser Lys Gly Asp Arg Ile Ala Gln Leu Leu Leu Leu Pro Asp Asn Thr
65                  70                  75                  80

Arg Glu Lys Ser Ala Gly Pro Glu Ile Lys Lys Met Gly Ser Ser Gly
                85                  90                  95

Asn Asp Ser Ala Tyr Leu Val Val Ser Leu Asn Asp Arg Pro Lys Leu
            100                 105                 110

Arg Leu Lys Ile Asn Gly Lys Glu Phe Glu Gly Ile Leu Asp Thr Gly
        115                 120                 125

Ala Asp Lys Ser Ile Ile Ser Thr His Trp Trp Pro Lys Ala Trp Pro
    130                 135                 140

Thr Thr Glu Ser Ser His Ser Leu Gln Gly Leu Gly Tyr Gln Ser Cys
145                 150                 155                 160

Pro Thr Ile Ser Ser Val Ala Leu Thr Trp Glu Ser Ser Glu Gly Gln
                165                 170                 175

Gln Gly Lys Phe Ile Pro Tyr Val Leu Pro Leu Pro Val Asn Leu Trp
            180                 185                 190

Gly Arg Asp Ile Met Gln His Leu Gly Leu Ile Leu Ser Asn Glu Asn
        195                 200                 205

Ala Pro Ser Gly Gly Tyr Ser Ala Lys Ala Lys Asn Ile Met Ala Lys
    210                 215                 220

Met Gly Tyr Lys Glu Gly Lys Gly Leu Gly His Gln Glu Gln Gly Arg
225                 230                 235                 240

Ile Glu Pro Ile Ser Pro Asn Gly Asn Gln Asp Arg Gln Gly Leu Gly
                245                 250                 255

Phe Pro
```

<210> 4
<211> 805
<212> PRT
<213> Mus musculus

<220>
<223> IAP sequence amino acid sequence (pol)

<400> 4

```
Met Asn Leu Phe Gly Pro Val Gln Arg Gly Leu Pro Val Leu Ser Ala
1               5                  10                  15

Leu Pro Arg Gly Trp Asn Leu Ile Ile Ile Asp Ile Lys Asp Cys Phe
            20                  25                  30

Phe Ser Ile Pro Leu Cys Pro Arg Asp Arg Pro Arg Phe Ala Phe Thr
        35                  40                  45

Ile Pro Ser Ile Asn His Met Glu Pro Asp Lys Arg Tyr Gln Trp Lys
    50                  55                  60

Val Leu Pro Gln Gly Met Ser Asn Ser Pro Thr Met Cys Gln Leu Tyr
65                  70                  75                  80

Val Gln Glu Ala Leu Leu Pro Val Arg Glu Gln Phe Pro Ser Leu Ile
                85                  90                  95

Leu Leu Leu Tyr Met Asp Asp Ile Leu Leu Cys His Lys Asp Leu Thr
            100                 105                 110

Met Leu Gln Lys Ala Tyr Pro Phe Leu Leu Lys Thr Leu Ser Gln Trp
        115                 120                 125

Gly Leu Gln Ile Ala Thr Glu Lys Val Gln Ile Ser Asp Thr Gly Gln
    130                 135                 140

Phe Leu Gly Ser Val Val Ser Pro Asp Lys Ile Val Pro Gln Lys Val
145                 150                 155                 160

Glu Ile Arg Arg Asp His Leu His Thr Leu Asn Asp Phe Gln Lys Leu
                165                 170                 175

Leu Gly Asp Ile Asn Trp Leu Arg Pro Phe Leu Lys Ile Pro Ser Ala
            180                 185                 190

Glu Leu Arg Pro Leu Phe Ser Ile Leu Glu Gly Asp Pro His Ile Ser
        195                 200                 205

Ser Pro Arg Thr Leu Thr Leu Ala Ala Asn Gln Ala Leu Gln Lys Val
    210                 215                 220
```

```
Glu Lys Ala Leu Gln Asn Ala Gln Leu Gln Arg Ile Glu Asp Ser Gln
225                 230                 235                 240

Pro Phe Ser Leu Cys Val Phe Lys Thr Ala Gln Leu Pro Thr Ala Val
                245                 250                 255

Leu Trp Gln Asn Gly Pro Leu Leu Trp Ile His Pro Asn Val Ser Pro
            260                 265                 270

Ala Lys Ile Ile Asp Trp Tyr Pro Asp Ala Ile Ala Gln Leu Ala Leu
        275                 280                 285

Lys Gly Leu Lys Ala Ala Ile Thr His Phe Gly Gln Ser Pro Tyr Leu
    290                 295                 300

Leu Ile Val Pro Tyr Thr Ala Ala Gln Val Gln Thr Leu Ala Ala Ala
305                 310                 315                 320

Ser Asn Asp Trp Ala Val Leu Val Thr Ser Phe Ser Gly Lys Ile Asp
                325                 330                 335

Asn His Tyr Pro Lys His Pro Ile Leu Gln Phe Ala Gln Asn Gln Ser
            340                 345                 350

Val Val Phe Pro Gln Ile Thr Val Arg Asn Pro Leu Lys Asn Gly Ile
        355                 360                 365

Val Val Tyr Thr Asp Gly Ser Lys Thr Gly Ile Gly Ala Tyr Val Ala
    370                 375                 380

Asn Gly Lys Val Val Ser Lys Gln Tyr Asn Glu Asn Ser Pro Gln Val
385                 390                 395                 400

Val Glu Cys Leu Val Val Leu Glu Val Leu Lys Thr Phe Leu Lys Pro
                405                 410                 415

Leu Asn Ile Val Ser Asp Ser Cys Tyr Val Val Asn Ala Val Asn Leu
            420                 425                 430

Leu Glu Val Ala Gly Val Ile Lys Pro Ser Ser Arg Val Ala Asn Ile
        435                 440                 445

Phe Gln Gln Ile Gln Leu Val Leu Leu Ser Arg Arg Ser Pro Val Tyr
    450                 455                 460
```

```
Ile Thr His Val Arg Ala His Ser Gly Leu Pro Gly Pro Met Ala Leu
465                 470                 475                 480

Gly Asn Asp Leu Ala Asp Lys Ala Thr Lys Val Val Ala Ala Ala Leu
                485                 490                 495

Ser Ser Pro Val Glu Ala Ala Arg Asn Phe His Asn Asn Phe His Val
            500                 505                 510

Thr Ala Glu Thr Leu Arg Ser Arg Phe Ser Leu Thr Arg Lys Glu Ala
        515                 520                 525

Arg Asp Ile Val Thr Gln Cys Gln Ser Cys Cys Glu Phe Leu Pro Val
    530                 535                 540

Pro His Val Gly Ile Asn Pro Arg Gly Ile Arg Pro Leu Gln Val Trp
545                 550                 555                 560

Gln Met Asp Val Thr His Val Ser Ser Phe Gly Lys Leu Gln Tyr Leu
                565                 570                 575

His Val Ser Ile Asp Thr Cys Ser Gly Ile Met Phe Ala Ser Pro Leu
            580                 585                 590

Thr Gly Glu Lys Ala Ser His Val Ile Gln His Cys Leu Glu Ala Trp
        595                 600                 605

Ser Ala Trp Gly Lys Pro Arg Leu Leu Lys Thr Asp Asn Gly Pro Ala
    610                 615                 620

Tyr Thr Ser Gln Lys Phe Gln Gln Phe Cys Arg Gln Met Asp Val Thr
625                 630                 635                 640

His Leu Thr Gly Leu Pro Tyr Asn Pro Gln Gly Gln Gly Ile Val Glu
                645                 650                 655

Arg Ala His Arg Thr Leu Lys Ala Tyr Leu Ile Lys Gln Lys Arg Gly
            660                 665                 670

Thr Phe Glu Glu Thr Val Pro Arg Ala Pro Arg Val Ser Val Ser Leu
        675                 680                 685

Ala Leu Phe Thr Leu Asn Phe Leu Asn Ile Asp Ala His Gly His Thr
    690                 695                 700

Ala Ala Glu Arg His Cys Ser Glu Pro Asp Arg Pro Asn Glu Met Val
```

705 710 715 720

Lys Trp Lys Asn Val Leu Asp Asn Lys Trp Tyr Gly Pro Asp Pro Ile
725 730 735

Leu Ile Arg Ser Arg Gly Ala Ile Cys Val Phe Pro Gln Asn Glu Asp
740 745 750

Asn Pro Phe Trp Val Pro Glu Arg Leu Thr Arg Lys Ile Gln Thr Asp
755 760 765

Gln Gly Asn Thr Asn Val Pro Arg Leu Gly Asp Val Gln Gly Val Asn
770 775 780

Asn Lys Glu Arg Ala Ala Leu Gly Asp Asn Val Asp Ile Ser Thr Pro
785 790 795 800

Asn Asp Gly Asp Val
805

<210> 5
<211> 673
<212> DNA
<213> Mus musculus

<220>
<223> CMV promoter sequence

<400> 5
tggccattgc atacgttgta tccatatcat aatatgtaca tttatattgg ctcatgtcca 60

acattaccgc catgttgaca ttgattattg actagttatt aatagtaatc aattacgggg 120

tcattagttc atagcccata tatggagttc cgcattacat aacttacggt aaatggcccg 180

cctggctgac cgcccaacga cccccgccca ttgacgtcaa taatgacgta tgttcccata 240

gtaacgccaa tagggacttt ccattgacgt caatgggtgg agtatttacg gtaaactgcc 300

cacttggcag tacatcaagt gtatcatatg ccaagtacgc cccctattga cgtcaatgac 360

ggtaaatggc ccgcctggca ttatgcccag tacatgacct tatgggactt tcctacttgg 420

cagtacatct acgtattagt catcgctatt accatggtga tgcggttttg gcagtacatc 480

aatgggcgtg gatagcggtt tgactcacgg ggatttccaa gtctccaccc cattgacgtc 540

aatgggagtt tgttttggca ccaaaatcaa cgggactttc caaaatgtcg taacaactcc 600

gccccattga cgcaaatggg cggtaggcgt gtacggtggg aggtctatat aagcagagct 660

cgtttagtga acc 673

<210> 6
<211> 655
<212> DNA
<213> Mus musculus

<220>
<223> CA1 promoter sequence (without the R region and with two bases deletion in the promoter region in addition thereto)

<400> 6
attgattatt gactagttat taatagtaat caattacggg gtcattagtt catagcccat 60

atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga ccgcccaacg 120

acccccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca atagggactt 180

tccattgacg tcaatgggtg gactatttac ggtaaactgc ccacttggca gtacatcaag 240

tgtatcatat gccaagtacg ccccctattg acgtcaatga cggtaaatgg cccgcctggc 300

attatgccca gtacatgacc ttatgggact ttcctacttg gcagtacatc tacgtattag 360

tcatcgctat taccatgggt cgaggtgagc cccacgttct gcttcactct ccccatctcc 420

cccccctccc caccccccaat tttgtattta tttatttttt aattattttg tgcagcgatg 480

ggggcggggg gggggggggc gcgcgccagg cggggcgggg cggggcgagg ggcggggcgg 540

ggcgaggcgg agaggtgcgg cggcagccaa tcagagcggc gcgctccgaa agtttccttt 600

tatggcgagg cggcggcggc ggcggcccta taaaaagcga agcgcgcggc gggcg 655

<210> 7
<211> 657
<212> DNA
<213> Mus musculus

<220>
<223> CA2 promoter sequence (without the R region)

<400> 7
attgattatt gactagttat taatagtaat caattacggg gtcattagtt catagcccat 60

atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga ccgcccaacg 120

acccccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca atagggactt 180

tccattgacg tcaatgggtg gactatttac ggtaaactgc ccacttggca gtacatcaag 240

tgtatcatat gccaagtacg ccccctattg acgtcaatga cggtaaatgg cccgcctggc 300

attatgccca gtacatgacc ttatgggact ttcctacttg gcagtacatc tacgtattag 360

tcatcgctat taccatgggt cgaggtgagc cccacgttct gcttcactct ccccatctcc 420

cccccctccc caccccccaat tttgtattta tttatttttt aattattttg tgcagcgatg 480

ggggcggggg gggggggggc gcgcgccagg cggggcgggg cggggcgagg ggcggggcgg 540

ggcgaggcgg agaggtgcgg cggcagccaa tcagagcggc gcgctccgaa agtttccttt 600

tatggcgagg cggcggcggc ggcggcccta taaaaagcga agcgcgcggc gggcggg 657

<210> 8
<211> 278
<212> DNA
<213> Gallus gallus

<220>
<223> avian beta-actin promoter sequence

<400> 8
tcgaggtgag ccccacgttc tgcttcactc tccccatctc ccccccctcc ccacccccaa 60

ttttgtattt atttatttttt taattatttt gtgcagcgat gggggcgggg ggggggggg 120

cgcgcgccag gcggggcggg gcggggcgag gggcggggcg gggcgaggcg gagaggtgcg 180

gcggcagcca atcagagcgg cgcgctccga aagtttcctt ttatggcgag gcggcggcgg 240

cggcggccct ataaaaagcg aagcgcgcgg cgggcggg 278

<210> 9
<211> 41
<212> DNA
<213> Mus musculus

<220>
<223> forward primer sequence for isolation of the IAP element used in Example 1

<400> 9
gcagcggccg ccgtggtggc acacactttt agtccccgca g 41

<210> 10
<211> 41
<212> DNA
<213> Mus musculus

<220>
<223> reverse primer sequence for isolation of the IAP element used in Example 1

<400> 10
ggcgcactag tgatgccctc tcaggcctcc actcaggcac t 41

<210> 11
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> forward primer sequence for isolation of the full length of the IAP element used in Example 1

<400> 11
atgcccagat ttcttccacg gctattaggg 30

<210> 12
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> reverse primer sequence for isolation of the full length of the IAP element used in Example 1

<400> 12
gatgccctct caggcctcca ctcaggcact 30

<210> 13
<211> 40
<212> DNA
<213> Mus musculus

<220>
<223> forward primer sequence related to the CMV promoter used in Example 1 (c)

<400> 13
ccaagcggcc gctggccatt gcatacgttg tatccatatc 40

<210> 14
<211> 40
<212> DNA
<213> Mus musculus

<220>
<223> reverse primer sequence related to the CMV promoter used in Example 1 (c)

<400> 14
gcgagaaaaa cggttcacta aacgagctct gcttatatag 40

<210> 15
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> forward primer sequence related to the R region of the IAP used in Example 1 (c)

<400> 15
ttagtgaacc gtttttctcg ctctcttgct 30

<210> 16
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> reverse primer sequence related to the R region of the IAP used

in Example 1 (c)

<400> 16
tctgaaatga agtatccctc ctgcgccagt 30

<210> 17
<211> 63
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of a linker DNA used in Example 3

<400> 17
cgaatcgtaa ccgttcgtac gagaattcgt acgagaatcg ctgtcctctc caacgagcca 60

agg 63

<210> 18
<211> 26
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of a linker DNA used in Example 3

<400> 18
ccttggctcg ttttttttg caaaaa 26

<210> 19
<211> 25
<212> DNA
<213> Mus musculus

<220>
<223> a linker specific primer for use in the first round
in Example 3 (forward)

<400> 19
cgaatcgtaa ccgttcgtac gagaa 25

<210> 20
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> a linker specific primer for use in the first round
in Example 3 (reverse)

<400> 20
gagatgcatg ctttgcatac ttctgcctgc 30

<210> 21
<211> 25
<212> DNA

<213> Mus musculus

<220>
<223> a linker specific primer for use in the second round
in Example 3 (forward)

<400> 21
tcgtacgaga atcgctgtcc tctcc 25

<210> 22
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of neo cassette specific primer for use
in the second round in Example 3 (reverse)

<400> 22
ggagcctggg gactttccac acctggttgc 30

<210> 23
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> an alternative linking sequence of neo cassette specific primer
for use in the second round in Example 3 (reverse)

<400> 23
ggggagcctg gggactttcc acaccctaac 30

<210> 24
<211> 39
<212> DNA
<213> Gallus gallus

<220>
<223> a primer 5' upstream until the transcription initiation site of
chicken beta-actin promoter used in Example 4

<400> 24
gcaatgcggc cgcattgatt attgactagt tattaatag 39

<210> 25
<211> 39
<212> DNA
<213> Gallus gallus

<220>
<223> a primer 3' of chicken beta-actin promoter used in Example 4

<400> 25
cgagaaaaac cgcccgccgc gcgcttcgct ttttatagg 39

<210> 26
<211> 40
<212> DNA
<213> Gallus gallus

<220>
<223> an alternative primer 3' of chicken beta-actin promoter used in Example 4

<400> 26
cgagaaaaac cccgcccgcc gcgcgcttcg ctttttatag 40

<210> 27
<211> 36
<212> DNA
<213> Mus musculus

<220>
<223> a primer of the 5' upstream from the 5' terminus of the R region of the IAP to the downstream of the U5 region used in Example 4

<400> 27
cgcggcgggc ggtttttctc gctctcttgc ttcttg 36

<210> 28
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> a primer of the 3' side from the 5' terminus of the R region of the IAP to the downstream of the U5 region used in Example 4

<400> 28
tctgaaatga agtatccctc ctgcgccagt 30

<210> 29
<211> 36
<212> DNA
<213> Mus musculus

<220>
<223> an alternative primer of the 3' side from the 5' terminus of the R region of the IAP to the downstream of the U5 region used in Example 4

<400> 29
cggcgggcgg ggtttttctc gctctcttgc ttcttg 36

<210> 30
<211> 903
<212> DNA
<213> Mus musculus

<220>
<223> gamma globin intron sequence

<400> 30
gtgagtccag gagatgtttc agcactgttg cctttagtct cgaggcaact tagacaactg 60

agtattgatc tgagcacagc agggtgtgag ctgtttgaag atactggggt tgggggtgaa 120

gaaactgcag aggactaact gggctgagac ccagtggcaa tgttttaggg cctaaggaat 180

gcctctgaaa atctagatgg acaactttga ctttgagaaa agagaggtgg aaatgaggaa 240

aatgactttt ctttattaga tttcggtaga aagaactttc acctttcccc tatttttgtt 300

attcgtttta aaacatctat ctggaggcag gacaagtatg gtcgttaaaa agatgcaggc 360

agaaggcata tattggctca gtcaaagtgg gggaactttg gtggccaaac atacattgct 420

aaggctattc ctatatcagc tggacacata taaaatgctg ctaatgcttc attacaaact 480

tatatccttt aattccagat gggggcaaag tatgtccagg ggtgaggaac aattgaaaca 540

tttgggctgg agtagatttt gaaagtcagc tctgtgtgtg tgtgtgtgtg tgtgtgtgtg 600

tgtgtgtgcg cgcacgtgtg tttgtgtgtg tgtgagagcg tgtgtttctt ttaacgtttt 660

cagcctacag catacagggt tcatggtggc aagaagataa caagatttaa attatggcca 720

gtgactagtg ctgcaagaag aacaactacc tgcatttaat gggaaagcaa aatctcaggc 780

tttgagggaa gttaacatag gcttgattct gggtggaagc tgggtgtgta gttatctgga 840

ggccaggctg gagctctcag ctcactatgg gttcatcttt attgtctcct ttcatctcaa 900

cag 903

<210> 31
<211> 15
<212> DNA
<213> Mus musculus

<220>
<223> a sequence of the tRNA binding site of the full length IAP

<400> 31
tccgggacga gaaaa 15

<210> 32
<211> 15
<212> DNA
<213> Mus musculus

<220>
<223> a repeat sequence of the R region of the full length IAP

<400> 32
ttgcttcttg ctctc 15

<210> 33
<211> 17
<212> DNA

<213> Mus musculus

<220>
<223> a specific sequence for the full length IAP (tRNA binding site)

<400> 33
tggtgccgaa ttccggg 17

<210> 34
<211> 15
<212> DNA
<213> Mus musculus

<220>
<223> a tandem repeat sequence specific for the full length IAP

<400> 34
aatccgggac gagaa 15

<210> 35
<211> 11
<212> DNA
<213> Mus musculus

<220>
<223> a repeat sequence of the R region found in the full length IAP

<400> 35
ttgcttcttg c 11

<210> 36
<211> 378
<212> DNA
<213> Mus musculus

<220>
<223> cytomegalovirus (CMV) enhancer sequence

<400> 36
attgattatt gactagttat taatagtaat caattacggg gtcattagtt catagcccat 60

atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga ccgcccaacg 120

acccccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca atagggactt 180

tccattgacg tcaatgggtg gagtatttac ggtaaactgc ccacttggca gtacatcaag 240

tgtatcatat gccaagtacg ccccctattg acgtcaatga cggtaaatgg cccgcctggc 300

attatgccca gtacatgacc ttatgggact ttcctacttg gcagtacatc tacgtattag 360

tcatcgctat taccatgg 378

<210> 37
<211> 30
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence in the sense direction of 1st primer used in Example 8

<400> 37
agggctgcgg caagggcaac atcctgttcg 30

<210> 38
<211> 30
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence in the antisense direction of 1st primer used in Example 8

<400> 38
gccgccgtcc tccacgtagg tcttctccag 30

<210> 39
<211> 30
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence in the sense direction of 2nd primer used in Example 8

<400> 39
ggcaaccagc tggtgcagat ccgcgtgacc 30

<210> 40
<211> 30
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence in the antisense direction of 2nd primer used in Example 8

<400> 40
gtccttcacc acgcccttgc tcttcatcag 30